



TRANSLATOR'S DECLARATION

I, Janet Hope, BSc.(Hons.), MIL., MITI., translator to Messrs. Taylor & Meyer of 20 Kingsmead Road, London, SW2 3JD, Great Britain, verify that I know well both the German and the English language, that I have prepared the attached English translation of        pages of a German Patent application in the German language with the title:

Neue für das lysR2-Gen kodierende Nukleotidsequenzen

identified by the code number 000181 BT / IP at the upper left of each page and that the attached English translation of this document is a true and correct translation of the document attached thereto to the best of my knowledge and belief.

I further declare that all statements made of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements are made with the knowledge that wilful false statements and the like are punishable by fine or imprisonment, or both, under 18 USC 1001, and that such false statements may jeopardize the validity of this document.

By: 

Date: 13/04/2001

**New nucleotide sequences which code for the lysR2 gene**

The invention provides nucleotide sequences from coryneform bacteria which code for the lysR2 gene and a process for the fermentative preparation of amino acids, in particular 5 L-lysine and L-valine, by attenuation of the lysR2 gene. The lysR2 gene codes for the LysR2 protein, which is a transcription regulator of the LysR family.

Prior art

L-Amino acids, in particular L-lysine and L-valine, are 10 used in human medicine and in the pharmaceuticals industry, in the foodstuffs industry and very particularly in animal nutrition.

It is known that amino acids are prepared by fermentation from strains of coryneform bacteria, in particular 15 *Corynebacterium glutamicum*. Because of their great importance, work is constantly being undertaken to improve the preparation processes. Improvements to the process can relate to fermentation measures, such as, for example, stirring and supply of oxygen, or the composition of the 20 nutrient media, such as, for example, the sugar concentration during the fermentation, or the working up to the product form by, for example, ion exchange chromatography, or the intrinsic output properties of the microorganism itself.

25 Methods of mutagenesis, selection and mutant selection are used to improve the output properties of these microorganisms. Strains which are resistant to antimetabolites or are auxotrophic for metabolites of regulatory importance and which produce amino acids are 30 obtained in this manner.

Methods of the recombinant DNA technique have also been employed for some years for improving the strain of *Corynebacterium* strains which produce L-amino acids.

#### Object of the invention

5 The inventors had the object of providing new measures for improved fermentative preparation of amino acids, in particular L-lysine and L-valine.

#### Description of the invention

The invention provides an isolated polynucleotide from 10 *coryneform* bacteria, comprising a polynucleotide sequence which codes for the *lysR2* gene, chosen from the group consisting of

- a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a 15 polypeptide which comprises the amino acid sequence of SEQ ID No. 2,
- b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of 20 SEQ ID No. 2,
- c) polynucleotide which is complementary to the polynucleotides of a) or b), and
- d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) 25 or c),

the polypeptide preferably having the activity of the transcription regulator *LysR2*.

The invention also provides the abovementioned polynucleotide, this preferably being a DNA which is 30 capable of replication, comprising:

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(i) the nucleotide sequence shown in SEQ ID No.1 or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

5 (iii) at least one sequence which hybridizes with the sequences complementary to sequences (i) or (ii), and optionally

(iv) sense mutations of neutral function in (i) which do not modify the activity of the

10 protein/polypeptide.

The invention also provides

a) polynucleotides comprising at least 15 successive nucleotides chosen from the nucleotide sequence of SEQ ID No. 1 between positions 1 and 231,

15 b) polynucleotides comprising at least 15 successive nucleotides chosen from the nucleotide sequence of SEQ ID No. 1 between positions 232 and 1161,

c) polynucleotides comprising at least 15 successive nucleotides chosen from the nucleotide sequence of SEQ

20 ID No. 1 between positions 1162 and 1364.

The invention also provides:

a polynucleotide, in particular DNA, which is capable of replication and comprises the nucleotide sequence as shown in SEQ ID No.1;

25 a polynucleotide which codes for a polypeptide which comprises the amino acid sequence as shown in SEQ ID No. 2;

a vector containing parts of the polynucleotide according to the invention, but at least 15 successive nucleotides of the sequence claimed

and coryneform bacteria in which the lysR2 gene is  
5 attenuated, in particular by an insertion or deletion [sic]

The invention also provides polynucleotides which substantially comprise a polynucleotide sequence, which are obtainable by screening by means of hybridization of a 10 corresponding gene library, which comprises the complete gene with the polynucleotide sequence corresponding to SEQ ID No. 1, with a probe which comprises the sequence of the polynucleotide mentioned, according to SEQ ID No. 1 or a fragment thereof, and isolation of the DNA sequence 15 mentioned.

Polynucleotide sequences according to the invention are suitable as hybridization probes for RNA, cDNA and DNA, in order to isolate, in the full length, nucleic acids, or polynucleotides or genes which code for the LysR2 protein 20 or to isolate those nucleic acids or polynucleotides or genes which have a high similarity with the sequence of the lysR2 gene. They are also suitable for incorporation into so-called "arrays", "micro arrays" or "DNA [sic] chips in order to detect and determine the corresponding 25 polynucleotides [sic]

Polynucleotide sequences according to the invention are furthermore suitable as primers with the aid of which DNA of genes which code for the LysR2 protein can be prepared with the polymerase chain reaction (PCR).

30 Such oligonucleotides which serve as probes or primers comprise at least 25, 26, 27, 28, 29 or 30, preferably at least 20, 21, 22, 23 or 24, very particularly preferably at least 15, 16, 17, 18 or 19 successive nucleotides.

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Oligonucleotides with a length of at least 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40, or at least 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 nucleotides are also suitable.

Oligonucleotides with a length of at least 100, 150, 200, 250 or 300 nucleotides are optionally also suitable.

"Isolated" means separated out of its natural environment.

"Polynucleotide" in general relates to polyribonucleotides and polydeoxyribonucleotides, it being possible for these to be non-modified RNA or DNA or modified RNA or DNA.

10 The polynucleotides according to the invention include a polynucleotide according to SEQ ID No. 1 or a fragment prepared therefrom and also those which are at least 70% to 80%, preferably at least 81% to 85%, particularly preferably at least 86% to 90% and very particularly 15 preferably at least 91%, 93%, 95%, 97% or 99% identical to the polynucleotide according to SEQ ID No. 1 or a fragment prepared therefrom.

"Polypeptides" are understood as meaning peptides or proteins which comprise two or more amino acids bonded via 20 peptide bonds.

The polypeptides according to the invention include a polypeptide according to SEQ ID No. 2, in particular those with the biological activity of the LysR2 protein, and also those which are at least 70% to 80%, preferably at least 25 81% to 85% and in particular at least 86% to 90% and very particularly preferably at least 91%, 93%, 95%, 97% or 99% identical to the polypeptide according to SEQ ID No. 2 and have the activity mentioned.

The invention furthermore relates to a process for the  
30 fermentative preparation of amino acids chosen from the  
group consisting of L-asparagine, L-threonine, L-serine, L-  
glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-  
methionine, L-isoleucine, L-leucine, L-tyrosine, L-

phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine, in particular L-lysine and L-valine, using coryneform bacteria which in particular already produce amino acids and in which the nucleotide sequences which 5 code for the *lysR2* gene are attenuated, in particular eliminated or expressed at a low level.

The term "attenuation" in this connection describes the reduction or elimination of the intracellular activity of one or more enzymes (proteins) in a microorganism which are 10 coded by the corresponding DNA, for example by using a weak promoter or using a gene or allele which codes for a corresponding enzyme with a low activity or inactivates the corresponding gene or allele or enzyme (protein), and optionally combining these measures.

15 The microorganisms which the present invention provides can prepare amino acids, in particular L-lysine and L-valine, from glucose, sucrose, lactose, fructose, maltose, molasses, starch, cellulose or from glycerol and ethanol. They can be representatives of coryneform bacteria, in 20 particular of the genus *Corynebacterium*. Of the genus *Corynebacterium*, there may be mentioned in particular the species *Corynebacterium glutamicum*, which is known among experts for its ability to produce L-amino acids.

Suitable strains of the genus *Corynebacterium*, in 25 particular of the species *Corynebacterium glutamicum* (*C. glutamicum*), are in particular the known wild-type strains

*Corynebacterium glutamicum* ATCC13032

*Corynebacterium acetoglutamicum* ATCC15806

*Corynebacterium acetoacidophilum* ATCC13870

30 *Corynebacterium melassecola* ATCC17965

*Corynebacterium thermoaminogenes* FERM BP-1539

*Brevibacterium flavum* ATCC14067

*Brevibacterium lactofermentum* ATCC13869 and

*Brevibacterium divaricatum* ATCC14020

or L-amino acid-producing mutants or strains prepared therefrom, such as, for example, the L-lysine-producing strains

*Corynebacterium glutamicum* FERM-P 1709  
*Brevibacterium flavum* FERM-P 1708  
*Brevibacterium lactofermentum* FERM-P 1712  
*Corynebacterium glutamicum* FERM-P 6463  
*Corynebacterium glutamicum* FERM-P 6464  
*Corynebacterium glutamicum* DSM 58-1  
*Corynebacterium glutamicum* DG 52-5  
*Corynebacterium glutamicum* DSM 5715 and  
*Corynebacterium glutamicum* DSM 12866

or such as, for example, the L-valine-producing strains.

*Corynebacterium glutamicum* DSM 12455  
*Corynebacterium glutamicum* FERM-P 9325  
*Brevibacterium lactofermentum* FERM-P 9324  
*Brevibacterium lactofermentum* FERM-P 1763

The inventors have succeeded in isolating the new *lysR2* gene of *C. glutamicum* which codes for the LysR2 protein, 20 which is a transcription regulator of the LysR family.

To isolate the *lysR2* gene or also other genes of *C. glutamicum*, a gene library of this microorganism is first set up in *Escherichia coli* (*E. coli*). The setting up of gene libraries is described in generally known textbooks and handbooks. The textbook by Winnacker: *Gene und Klone, Eine Einführung in die Gentechnologie* [Genes and Clones, An Introduction to Genetic Engineering] (Verlag Chemie, Weinheim, Germany, 1990), or the handbook by Sambrook et al.: *Molecular Cloning, A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1989) may be mentioned as an example. A well-known gene library is that of the *E. coli* K-12 strain W3110 set up in  $\lambda$  vectors by Kohara et al. (Cell 50, 495 -508 (1987)). Bathe et al. (Molecular and General Genetics, 252:255-265, 1996) describe a gene

library of *C. glutamicum* ATCC13032, which was set up with the aid of the cosmid vector SuperCos I (Wahl et al., 1987, Proceedings of the National Academy of Sciences USA, 84:2160-2164) in the *E. coli* K-12 strain NM554 (Raleigh et al., 1988, Nucleic Acids Research 16:1563-1575). Börmann et al. (Molecular Microbiology 6(3), 317-326) (1992) in turn describe a gene library of *C. glutamicum* ATCC13032 using the cosmid pHC79 (Hohn and Collins, 1980, Gene 11, 291-298).

10 To prepare a gene library of *C. glutamicum* in *E. coli* it is also possible to use plasmids such as pBR322 (Bolivar, 1979, Life Sciences, 25, 807-818) or pUC9 (Vieira et al., 1982, Gene, 19:259-268). Suitable hosts are, in particular, those *E. coli* strains which are restriction-15 and recombination-defective, such as, for example, the strain DH5 $\alpha$  (Jeffrey H. Miller: "A Short Course in Bacterial Genetics, A Laboratory Manual and Handbook for Escherichia coli and Related Bacteria", Cold Spring Harbour [sic] Laboratory Press, 1992).

20 The long DNA fragments cloned with the aid of cosmids or other  $\lambda$  vectors can then be subcloned in turn into the usual vectors suitable for DNA sequencing.

Methods of DNA sequencing are described, inter alia, by Sanger et al. (Proceedings of the National Academy of Sciences of the United States of America USA, 74:5463-5467, 1977).

The resulting DNA sequences can then be investigated with known algorithms or sequence analysis programs, such as e.g. that of Staden (Nucleic Acids Research 14, 217-30 232(1986)), that of Marck (Nucleic Acids Research 16, 1829-1836 (1988)) or the GCG program of Butler (Methods of Biochemical Analysis 39, 74-97 (1998)).

The new DNA sequence of *C. glutamicum* which codes for the lysR2 gene and which, as SEQ ID No. 1, is a constituent of the present invention has been obtained in this manner. The amino acid sequence of the corresponding protein has 5 furthermore been derived from the present DNA sequence by the methods described above. The resulting amino acid sequence of the lysR2 gene product is shown in SEQ ID No. 2. It is known that enzymes endogenous in the host can split off the N-terminal amino acid methionine or 10 formylmethionine of the protein formed.

Coding DNA sequences which result from SEQ ID No. 1 by the degeneracy of the genetic code are also a constituent of the invention. In the same way, DNA sequences which hybridize with SEQ ID No. 1 or parts of SEQ ID No. 1 are a 15 constituent of the invention. Conservative amino acid exchanges, such as e.g. exchange of glycine for alanine or of aspartic acid for glutamic acid in proteins, are furthermore known among experts as "sense mutations" which do not lead to a fundamental change in the activity of the 20 protein, i.e. are of neutral function. It is furthermore known that changes on the N and/or C terminus of a protein cannot substantially impair or can even stabilize the function thereof. Information in this context can be found by the expert, inter alia, in Ben-Bassat et al. (Journal of 25 Bacteriology 169:751-757 (1987)), in O'Regan et al. (Gene 77:237-251 (1989)), in Sahin-Toth et al. (Protein Sciences 3:240-247 (1994)), in Hochuli et al. (Bio/Technology 6:1321-1325 (1988)) and in known textbooks of genetics and 30 molecular biology. Amino acid sequences which result in a corresponding manner from SEQ ID No. 2 are also a constituent of the invention.

Finally, DNA sequences which are prepared by the polymerase chain reaction (PCR) using primers which result from SEQ ID No. 1 are a constituent of the invention. Such

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oligonucleotides typically have a length of at least 15 nucleotides.

Instructions for identifying DNA sequences by means of hybridization can be found by the expert, inter alia, in 5 the handbook "The DIG System Users Guide for Filter Hybridization" from Boehringer Mannheim GmbH (Mannheim, Germany, 1993) and in Liebl et al. (International Journal of Systematic Bacteriology 41: 255-260 (1991)).

Instructions for amplification of DNA sequences with the 10 aid of the polymerase chain reaction (PCR) can be found by the expert, inter alia, in the handbook by Gait:

Oligonukleotide [sic] synthesis: A Practical Approach (IRL Press, Oxford, UK, 1984) and in Newton and Graham: PCR (Spektrum Akademischer Verlag, Heidelberg, Germany, 1994).

15 In the work on the present invention, it has been found that coryneform bacteria produce amino acids, in particular L-lysine and L-valine, in an improved manner after attenuation of the lysR2 gene.

To achieve an attenuation, either the expression of the 20 lysR2 gene or the catalytic properties of the enzyme protein can be reduced or eliminated. The two measures can optionally be combined.

The reduction in gene expression can take place by suitable culturing or by genetic modification (mutation) of the 25 signal structures of gene expression. Signal structures of gene expression are, for example, repressor genes, activator genes, operators, promoters, attenuators, ribosome binding sites, the start codon and terminators. The expert can find information on this e.g. in the patent application WO 96/15246, in Boyd and Murphy (Journal of Bacteriology 170: 5949 (1988)), in Voskuil and Chambliss (Nucleic Acids Research 26: 3548 (1998)), in Jensen and Hammer (Biotechnology and Bioengineering 58: 191 (1998)), in Pátek et al. (Microbiology 142: 1297 (1996)), Vasicova

et al. (Journal of Bacteriology 181: 6188 (1999)) and in known textbooks of genetics and molecular biology, such as e.g. the textbook by Knippers ("Molekulare Genetik [Molecular Genetics]", 6th edition, Georg Thieme Verlag, Stuttgart, Germany, 1995) or that by Winnacker ("Gene und Klone [Genes and Clones]", VCH Verlagsgesellschaft, Weinheim, Germany, 1990).

Mutations which lead to a change or reduction in the catalytic properties of enzyme proteins are known from the 10 prior art; examples which may be mentioned are the works by Qiu and Goodman (Journal of Biological Chemistry 272: 8611-8617 (1997)), Sugimoto et al. (Bioscience Biotechnology and Biochemistry 61: 1760-1762 (1997)) and Möckel ("Die Threoninehydratase aus Corynebacterium glutamicum: 15 Aufhebung der allosterischen Regulation und Struktur des Enzyms [Threonine dehydratase from Corynebacterium glutamicum: Cancelling the allosteric regulation and structure of the enzyme]", Reports from the Jülich Research Centre, JüL-2906, ISSN09442952, Jülich, Germany, 1994). 20 Summarizing descriptions can be found in known textbooks of genetics and molecular biology, such as e.g. that by Hagemann ("Allgemeine Genetik [General Genetics]", Gustav Fischer Verlag, Stuttgart, 1986).

Possible mutations are transitions, transversions, 25 insertions and deletions. Depending on the effect of the amino acid exchange on the enzyme activity, missense mutations or nonsense mutations are referred to. Insertions or deletions of at least one base pair (bp) in a gene lead to frame shift mutations, as a consequence of 30 which incorrect amino acids are incorporated or translation is interrupted prematurely. Deletions of several codons typically lead to a complete loss of the enzyme activity. Instructions on generation of such mutations are prior art and can be found in known textbooks of genetics and 35 molecular biology, such as e.g. the textbook by Knippers

("Molekulare Genetik [Molecular Genetics]", 6th edition, Georg Thieme Verlag, Stuttgart, Germany, 1995), that by Winnacker ("Gene und Klone [Genes and Clones]", VCH Verlagsgesellschaft, Weinheim, Germany, 1990) or that by 5 Hagemann ("Allgemeine Genetik [General Genetics]", Gustav Fischer Verlag, Stuttgart, 1986).

A common method of mutating genes of *C. glutamicum* is the method of gene disruption and gene replacement described by Schwarzer and Pühler (Bio/Technology 9, 84-87 (1991)).

10 In the method of gene disruption a central part of the coding region of the gene of interest is cloned in a plasmid vector which can replicate in a host (typically *E. coli*), but not in *C. glutamicum*. Possible vectors are, for example, pSUP301 (Simon et al., Bio/Technology 1, 784-791 15 (1983)), pK18mob or pK19mob (Schäfer et al., Gene 145, 69-73 (1994)), pK18mobsacB or pK19mobsacB (Jäger et al., Journal of Bacteriology 174: 5462-65 (1992)), pGEM-T (Promega corporation, Madison, WI, USA), pCR2.1-TOPO (Shuman (1994). Journal of Biological Chemistry 269:32678-20 84; US Patent 5,487,993), pCR®Blunt (Invitrogen, Groningen, The Netherlands; Bernard et al., Journal of Molecular Biology, 234: 534-541 (1993)) or pEM1 (Schrumpf et al, 1991, Journal of Bacteriology 173:4510-4516). The plasmid vector which contains the central part of the 25 coding region of the gene is then transferred into the desired strain of *C. glutamicum* by conjugation or transformation. The method of conjugation is described, for example, by Schäfer et al. (Applied and Environmental Microbiology 60, 756-759 (1994)). Methods for 30 transformation are described, for example, by Thierbach et al. (Applied Microbiology and Biotechnology 29, 356-362 (1988)), Dunican and Shivnan (Bio/Technology 7, 1067-1070 (1989)) and Tauch et al. (FEMS Microbiological Letters 123, 343-347 (1994)). After homologous recombination by means 35 of a "cross-over" event, the coding region of the gene in

question is interrupted by the vector sequence and two incomplete alleles are obtained, one lacking the 3' end and one lacking the 5' end. This method has been used, for example, by Fitzpatrick et al. (Applied Microbiology and Biotechnology 42, 575-580 (1994)) to eliminate the recA gene of *C. glutamicum*.

Figure 1 shows by way of example the plasmid vector pCR2.1lysR2int, with the aid of which the lysR2 gene can be disrupted or eliminated.

10 In the method of gene replacement, a mutation, such as e.g. a deletion, insertion or base exchange, is established in vitro in the gene of interest. The allele prepared is in turn cloned in a vector which is not replicative for *C. glutamicum* and this is then transferred into the desired 15 host of *C. glutamicum* by transformation or conjugation. After homologous recombination by means of a first "cross-over" event which effects integration and a suitable second "cross-over" event which effects excision in the target gene or in the target sequence, the incorporation of the 20 mutation or of the allele is achieved. This method was used, for example, by Peters-Wendisch et al. (Microbiology 144, 915 - 927 (1998)) to eliminate the pyc gene of *C. glutamicum* by a deletion.

A deletion, insertion or a base exchange can be 25 incorporated into the lysR2 gene in this manner.

In addition, it may be advantageous for the production of L-amino acids, in particular L-lysine and L-valine, to enhance, in particular to over-express, one or more enzymes of the particular biosynthesis pathway, of glycolysis, of 30 anaplerosis, of the pentose phosphate cycle or of amino acid export, in addition to attenuation of the lysR2 gene.

The term "enhancement" in this connection describes the increase in the intracellular activity of one or more

enzymes (proteins) in a microorganism which are coded by the corresponding DNA, for example by increasing the number of copies of the gene or genes, using a potent promoter or using a gene or allele which codes for a corresponding enzyme (protein) having a high activity, and optionally combining these measures.

Thus, for example, for the preparation of L-lysine, at the same time one or more of the genes chosen from the group consisting of

- 10 • the dapA gene which codes for dihydripicolinate synthase (EP-B 0 197 335),
- the eno gene which codes for enolase (DE: 19947791.4),
- the zwf gene which codes for the zwf gene product (JP-A-09224661),
- 15 • the pyc gene which codes for pyruvate carboxylase (Peters-Wendisch et al. (Microbiology 144, 915 - 927 (1998))
- the lysE gene which codes for lysine export (DE-A-195 48 222)
- 20 • the lysC gene which codes for a feed back resistant aspartate kinase (EP-B-0387527; EP-A-0699759)
- the zwal gene which codes for the Zwal protein (DE: 199 59 328.0, DSM 13115)

can be enhanced, in particular over-expressed.

25 Thus, for example, for the production of L-valine, at the same time one or more of the genes or alleles chosen from the group consisting of

- at the same time the ilvBN gene which codes for acetoxyhydroxy-acid synthase (Keilhauer et al., (1993) Journal of Bacteriology 175: 5595-5603), or
- at the same time the ilvD gene which codes for dihydroxy-acid dehydratase (Sahm and Eggeling (1999) Applied and Environmental Microbiology 65: 1973-1979), or
- at the same time the mgo gene which codes for malate:quinone oxidoreductase (Molenaar et al., European Journal of Biochemistry 254, 395-403 (1998))

10 can be enhanced, in particular over-expressed.

It may furthermore be advantageous for the production of amino acids, in particular L-lysine, in addition to the attenuation of the lysR2 gene, at the same time for one or more of the genes chosen from the group consisting of

- 15 • the pck gene which codes for phosphoenol pyruvate carboxykinase (DE 199 50 409.1, DSM 13047),
- the pgi gene which codes for glucose 6-phosphate isomerase (US 09/396,478, DSM 12969),
- the poxB gene which codes for pyruvate oxidase 20 (DE:1995 1975.7, DSM 13114)
- the zwa2 gene which codes for the Zwa2 protein (DE: 19959327.2, DSM 13113),

to be attenuated, in particular eliminated.

Finally, it may be advantageous for the production of L-25 lysine, in addition to the attenuation of the lysR2 gene, at the same time for one or more of the genes chosen from the group consisting of

- the hom gene which codes for homoserine dehydrogenase (EP-A -0131171),
- the thrB gene which codes for homoserine kinase (Peoples, O.W., et al., Molecular Microbiology 2 (1988): 63 - 72),  
5 and
- the panD gene which codes for aspartate decarboxylase (EP-A-1006192)

to be attenuated, in particular eliminated.

The attenuation of homoserine dehydrogenase can also be  
10 achieved, inter alia, by amino acid exchanges, such as, for example, by exchange of L-valine for L-alanine, L-glycine or L-leucine in position 59 of the enzyme protein, by exchange of L-valine by L-isoleucine, L-valine or L-leucine in position 104 of the enzyme protein and/or by exchange of  
15 L-asparagine by L-threonine or L-serine in position 118 of the enzyme protein.

The attenuation of homoserine kinase can also be achieved, inter alia, by amino acid exchanges, such as, for example, by exchange of L-alanine for L-valine, L-glycine or L-  
20 leucine in position 133 of the enzyme protein and/or by exchange of L-proline by L-threonine, L-isoleucine or L-serine in position 138 of the enzyme protein.

The attenuation of aspartate decarboxylase can also be achieved, inter alia, by amino acid exchanges, such as, for  
25 example, by exchanges of L-alanine for L-glycine, L-valine or L-isoleucine in position 36 of the enzyme protein.

In addition to attenuation of the lysR2 gene it may furthermore be advantageous, for the production of amino acids, in particular L-lysine and L-valine, to eliminate  
30 undesirable side reactions, (Nakayama: "Breeding of Amino Acid Producing Micro-organisms", in: Overproduction of

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Microbial Products, Krumphanzl, Sickyta, Vanek (eds.), Academic Press, London, UK, 1982).

The invention also provides the microorganisms prepared according to the invention, and these can be cultured 5 continuously or discontinuously in the batch process (batch culture) or in the fed batch (feed process) or repeated fed batch process (repetitive feed process) for the purpose of production of L-amino acids, in particular L-lysine and L-valine. A summary of known culture methods are [sic] 10 described in the textbook by Chmiel (Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess Technology 1. Introduction to Bioprocess Technology (Gustav Fischer Verlag, Stuttgart, 1991)) or in the textbook by Storhas (Bioreaktoren und peripherie Einrichtungen 15 [Bioreactors and Peripheral Equipment] (Vieweg Verlag, Braunschweig/Wiesbaden, 1994)).

The culture medium to be used must meet the requirements of the particular strains in a suitable manner. Descriptions of culture media for various microorganisms are contained 20 in the handbook "Manual of Methods for General Bacteriology" of the American Society for Bacteriology (Washington D.C., USA, 1981). Sugars and carbohydrates, such as e.g. glucose, sucrose, lactose, fructose, maltose, molasses, starch and cellulose, oils and fats, such as, for 25 example, soya oil, sunflower oil, groundnut oil and coconut fat, fatty acids, such as, for example, palmitic acid, stearic acid and linoleic acid, alcohols, such as, for example, glycerol and ethanol, and organic acids, such as, for example, acetic acid, can be used as the source of 30 carbon. These substances can be used individually or as a mixture.

Organic nitrogen-containing compounds, such as peptones, yeast extract, meat extract, malt extract, corn steep liquor, soya bean flour and urea, or inorganic compounds, 35 such as ammonium sulfate, ammonium chloride, ammonium

phosphate, ammonium carbonate and ammonium nitrate, can be used as the source of nitrogen. The sources of nitrogen can be used individually or as a mixture.

Phosphoric acid, potassium dihydrogen phosphate or 5 dipotassium hydrogen phosphate or the corresponding sodium-containing salts can be used as the source of phosphorus. The culture medium must furthermore comprise salts of metals, such as, for example, magnesium sulfate or iron sulfate, which are necessary for growth. Finally, 10 essential growth substances, such as amino acids and vitamins, can be employed in addition to the abovementioned substances. Suitable precursors can moreover be added to the culture medium. The starting substances mentioned can be added to the culture in the form of a single batch, or 15 can be fed in during the culture in a suitable manner.

Basic compounds, such as sodium hydroxide, potassium hydroxide, ammonia or aqueous ammonia, or acid compounds, such as phosphoric acid or sulfuric acid, can be employed in a suitable manner to control the pH of the culture.

20 Antifoams, such as, for example, fatty acid polyglycol esters, can be employed to control the development of foam. Suitable substances having a selective action, such as, for example, antibiotics, can be added to the medium to maintain the stability of plasmids. To maintain aerobic 25 conditions, oxygen or oxygen-containing gas mixtures, such as, for example, air, are introduced into the culture. The temperature of the culture is usually 20°C to 45°C, and preferably 25°C to 40°C. Culturing is continued until a maximum of the desired product has formed. This target is 30 usually reached within 10 hours to 160 hours.

Methods for the determination of L-amino acids are known from the prior art. The analysis can thus be carried out, for example, as described by Spackman et al. (Analytical Chemistry, 30, (1958), 1190) by anion exchange 35 chromatography with subsequent ninhydrin derivatization, or

it can be carried out by reversed phase HPLC, for example as described by Lindroth et al. (Analytical Chemistry (1979) 51: 1167-1174).

A pure culture of the following microorganism was deposited  
5 on 28th July 2000 at the Deutsche Sammlung für  
Mikroorganismen und Zellkulturen (DSMZ = German Collection  
of Microorganisms and Cell Cultures, Braunschweig, Germany)  
in accordance with the Budapest Treaty:

10 • Escherichia coli strain TOP10F/pCR2.1lysR2int as DSM  
13617.

The process according to the invention is used for the  
fermentative preparation of amino acids, in particular L-  
lysine and L-valine.

15 The present invention is explained in more detail in the  
following with the aid of embodiment examples.

The isolation of plasmid DNA from Escherichia coli and all  
techniques of restriction, Klenow and alkaline phosphatase  
treatment were carried out by the method of Sambrook et al.  
(Molecular Cloning. A Laboratory Manual (1989) Cold Spring  
20 Harbour [sic] Laboratory Press, Cold Spring Harbor, NY,  
USA). Methods for transformation of Escherichia coli are  
also described in this handbook.

25 The composition of the usual nutrient media, such as LB or  
TY medium, can also be found in the handbook by Sambrook et  
al.

#### Example 1

Preparation of a genomic cosmid gene library from C.  
glutamicum ATCC 13032

30 Chromosomal DNA from C. glutamicum ATCC 13032 was isolated  
as described by Tauch et al. (1995, Plasmid 33:168-179) and  
partly cleaved with the restriction enzyme Sau3AI (Amersham

Pharmacia, Freiburg, Germany, Product Description Sau3AI, Code no. 27-0913-02). The DNA fragments were dephosphorylated with shrimp alkaline phosphatase (Roche Molecular Biochemicals, Mannheim, Germany, Product 5 Description SAP, Code no. 1758250). The DNA of the cosmid vector SuperCos1 (Wahl et al., 1987, Proceedings of the National Academy of Sciences, USA 84:2160-2164), obtained from Stratagene (La Jolla, USA, Product Description SuperCos1 Cosmid Vector Kit, Code no. 251301) was cleaved 10 with the restriction enzyme XbaI (Amersham Pharmacia, Freiburg, Germany, Product Description XbaI, Code no. 27-0948-02) and likewise dephosphorylated with shrimp alkaline phosphatase.

The cosmid DNA was then cleaved with the restriction enzyme 15 BamHI (Amersham Pharmacia, Freiburg, Germany, Product Description BamHI, Code no. 27-0868-04). The cosmid DNA treated in this manner was mixed with the treated ATCC13032 DNA and the batch was treated with T4 DNA ligase (Amersham Pharmacia, Freiburg, Germany, Product Description T4-DNA- 20 Ligase, Code no. 27-0870-04). The ligation mixture was then packed in phages with the aid of Gigapack II XL Packing Extract (Stratagene, La Jolla, USA, Product Description Gigapack II XL Packing Extract, Code no. 200217).

For infection of the *E. coli* strain NM554 (Raleigh et al. 25 1988, Nucleic Acid Res. 16:1563-1575) the cells were taken up in 10 mM MgSO<sub>4</sub> and mixed with an aliquot of the phage suspension. The infection and titering of the cosmid library were carried out as described by Sambrook et al. (1989, Molecular Cloning: A laboratory Manual, Cold Spring 30 Harbor), the cells being plated out on LB agar (Lennox, 1955, Virology, 1:190) + 100 µg/ml ampicillin. After incubation overnight at 37°C, recombinant individual clones were selected.

Example 2

## Isolation and sequencing of the lysR2 gene

The cosmid DNA of an individual colony was isolated with the Qiaprep Spin Miniprep Kit (Product No. 27106, Qiagen, 5 Hilden, Germany) in accordance with the manufacturer's instructions and partly cleaved with the restriction enzyme Sau3AI (Amersham Pharmacia, Freiburg, Germany, Product Description Sau3AI, Product No. 27-0913-02). The DNA fragments were dephosphorylated with shrimp alkaline 10 phosphatase (Roche Molecular Biochemicals, Mannheim, Germany, Product Description SAP, Product No. 1758250). After separation by gel electrophoresis, the cosmid fragments in the size range of 1500 to 2000 bp were isolated with the QiaExII Gel Extraction Kit (Product No. 15 20021, Qiagen, Hilden, Germany).

The DNA of the sequencing vector pZero-1, obtained from Invitrogen (Groningen, The Netherlands, Product Description Zero Background Cloning Kit, Product No. K2500-01) was cleaved with the restriction enzyme BamHI (Amersham 20 Pharmacia, Freiburg, Germany, Product Description BamHI, Product No. 27-0868-04). The ligation of the cosmid fragments in the sequencing vector pZero-1 was carried out as described by Sambrook et al. (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor), the DNA mixture 25 being incubated overnight with T4 ligase (Pharmacia Biotech, Freiburg, Germany). This ligation mixture was then electroporated (Tauch et al. 1994, FEMS Microbiol Letters, 123:343-7) into the *E. coli* strain DH5 $\alpha$ MCR (Grant, 1990, Proceedings of the National Academy of 30 Sciences, U.S.A., 87:4645-4649) and plated out on LB agar (Lennox, 1955, Virology, 1:190) with 50  $\mu$ g/ml zeocin.

The plasmid preparation of the recombinant clones was carried out with Biorobot 9600 (Product No. 900200, Qiagen, Hilden, Germany). The sequencing was carried out by the

dideoxy chain termination method of Sanger et al. (1977, Proceedings of the National Academies of Sciences, U.S.A., 74:5463-5467) with modifications according to Zimmerman et al. (1990, Nucleic Acids Research, 18:1067). The "RR 5 dRhodamin Terminator Cycle Sequencing Kit" from PE Applied Biosystems (Product No. 403044, Weiterstadt, Germany) was used. The separation by gel electrophoresis and analysis of the sequencing reaction were carried out in a "Rotiphoresis NF Acrylamide/Bisacrylamide" Gel (29:1) 10 (Product No. A124.1, Roth, Karlsruhe, Germany) with the "ABI Prism 377" sequencer from PE Applied Biosystems (Weiterstadt, Germany).

The raw sequence data obtained were then processed using the Staden program package (1986, Nucleic Acids Research, 15 14:217-231) version 97-0. The individual sequences of the pZero1 derivatives were assembled to a continuous contig. The computer-assisted coding region analysis [sic] were prepared with the XNIP program (Staden, 1986, Nucleic Acids Research, 14:217-231). Further analyses were carried out 20 with the "BLAST search program" (Altschul et al., 1997, Nucleic Acids Research, 25:3389-3402) against the non-redundant databank of the "National Center for Biotechnology Information" (NCBI, Bethesda, MD, USA).

The resulting nucleotide sequence is shown in SEQ ID No. 1. 25 Analysis of the nucleotide sequence showed an open reading frame of 933 base pairs, which was called the lysR2 gene. The lysR2 gene codes for a polypeptide of 310 amino acids.

404270 60692850

Example 3

Preparation of an integration vector for integration mutagenesis of the lysR2 gene

From the strain ATCC 13032, chromosomal DNA was isolated by 5 the method of Eikmanns et al. (Microbiology 140: 1817 - 1828 (1994)). On the basis of the sequence of the lysR2 gene known for *C. glutamicum* from example 2, the following oligonucleotides were chosen for the polymerase chain reaction (see SEQ ID No. 4 and SEQ ID No. 5):

10 lysR2intA:  
5'CCA TCG TCG CAG AAT TCA AC 3'  
lysR2intB:  
5'GCT TCT TCG GCT AAT GCA TC 3'

The primers shown were synthesized by MWG Biotech 15 (Ebersberg, Germany) and the PCR reaction was carried out by the standard PCR method of Innis et al. (PCR protocols. A guide to methods and applications, 1990, Academic Press) with Pwo-Polymerase from Boehringer. With the aid of the 20 polymerase chain reaction, an internal fragment of the lysR2 gene 439 bp in size was isolated, this being shown in SEQ ID No. 3.

The amplified DNA fragment was ligated with the TOPO TA 25 Cloning Kit from Invitrogen Corporation (Carlsbad, CA, USA; Catalogue Number K4500-01) in the vector pCR2.1-TOPO (Mead et al. (1991) Bio/Technology 9:657-663).

The *E. coli* strain TOP10F was then transformed with the 30 ligation batch (Hanahan, In: DNA cloning. A practical approach. Vol. I, IRL-Press, Oxford, Washington DC, USA, 1985). Selection of plasmid-carrying cells was made by plating out the transformation batch on LB agar (Sambrook et al., Molecular cloning: A Laboratory Manual. 2<sup>nd</sup> Ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), which had been supplemented with 25 mg/l

kanamycin. Plasmid DNA was isolated from a transformant with the aid of the QIAprep Spin Miniprep Kit from Qiagen and checked by restriction with the restriction enzyme EcoRI and subsequent agarose gel electrophoresis (0.8%).

5 The plasmid was called pCR2.1lysR2int.

Example 4

Integration mutagenesis of the lysR2 gene in the lysine producer DSM 5715 and in the valine producer FERM BP-1763

The vector pCR2.1lysR2int mentioned in example 3 was 10 electroporated by the electroporation method of Tauch et al. (FEMS Microbiological Letters, 123:343-347 (1994)) into Corynebacterium glutamicum DSM 5715 and Brevibacterium lactofermentum FERM BP-1763. The strain DSM 5715 is an AEC-resistant lysine producer (EP-B-435 132). The strain 15 FERM BP-1763 is a valine producer in need of isoleucine and methionine (US-A-5,188,948). The vector pCR2.1lysR2int cannot replicate independently in DSM 5715 or FERM BP-1763 and is retained in the cell only if it has integrated into the chromosome of DSM 5715 or FERM BP-1763. Selection of 20 clones with pCR2.1lysR2int integrated into the chromosome was carried out by plating out the electroporation batch on LB agar (Sambrook et al., Molecular Cloning: A Laboratory Manual. 2<sup>nd</sup> Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.), which had been supplemented with 25 15 mg/l kanamycin.

For detection of the integration, the lysR2int fragment was labelled with the Dig hybridization kit from Boehringer by the method of "The DIG System Users Guide for Filter Hybridization" of Boehringer Mannheim GmbH (Mannheim, 30 Germany, 1993). Chromosomal DNA of a potential integrant was isolated by the method of Eikmanns et al. (Microbiology 140: 1817 - 1828 (1994)) and in each case cleaved with the restriction enzymes SalI, SacI and HindIII. The fragments formed were separated by agarose gel electrophoresis and

hybridized at 68°C with the Dig hybridization [sic] kit from Boehringer. The plasmid pCR2.1lysR2int mentioned in example 3 had been inserted into the chromosome of DSM 5715 and FERM BP-1763 within the chromosomal lysR2 gene. The 5 strains were called DSM5715::pCR2.1lysR2int and FERM BP-1763::pCR2.1lysR2int.

Example 5

Preparation of L-lysine and L-valine

The C. glutamicum and B. lactofermentum strains

10 DSM5715::pCR2.1lysR2int and FERM BP-1763::pCR2.1lysR2int obtained in example 4 were cultured in a nutrient medium suitable for the production of L-lysine and L-valine and the L-lysine and L-valine content in the culture supernatant was determined.

15 For this, the strains were first incubated on an agar plate with the corresponding antibiotic (brain-heart agar with kanamycin (25 mg/l) [sic] for 24 hours at 33°C. Starting from this agar plate culture, a preculture was seeded (10 ml medium in a 100 ml conical flask). The complete 20 medium CgIII was used as the medium for the preculture.

Medium Cg III

NaCl 2.5 g/l

Bacto-Peptone 10 g/l

Bacto-Yeast extract 10 g/l

Glucose (autoclaved separately) 2% (w/v)

The pH was brought to pH 7.4

Kanamycin (25 mg/l) was added to this. The preculture was incubated for 24 hours at 33°C at 240 rpm on a shaking machine. A main culture was seeded from this preculture such that the initial OD (660 nm) of the main culture was 5 0.1 OD. Medium MM was used for the main culture.

## Medium MM

CSL (corn steep liquor)	5 g/l
MOPS	20 g/l
Glucose (autoclaved separately)	50g/l
Salts:	
(NH <sub>4</sub> ) <sub>2</sub> SO <sub>4</sub> ) [sic]	25 g/l
KH <sub>2</sub> PO <sub>4</sub>	0.1 g/l
MgSO <sub>4</sub> * 7 H <sub>2</sub> O	1.0 g/l
CaCl <sub>2</sub> * 2 H <sub>2</sub> O	10 mg/l
FeSO <sub>4</sub> * 7 H <sub>2</sub> O	10 mg/l
MnSO <sub>4</sub> * H <sub>2</sub> O	5.0mg/l
Biotin (sterile-filtered)	0.3 mg/l
Thiamine * HCl (sterile-filtered)	0.2 mg/l
CaCO <sub>3</sub>	25 g/l

The CSL, MOPS and the salt solution are brought to pH 7 with aqueous ammonia and autoclaved. The sterile substrate and vitamin solutions are then added, as well as the CaCO<sub>3</sub> autoclaved in the dry state. For culturing of DSM 5715,

0.1 g/l leucine was additionally added to the medium. For culturing of FERM BP-1763, 0.1 g/l isoleucine and 0.1 g/l methionine were additionally added to the medium.

Culturing is carried out in a 10 ml volume in a 100 ml 5 conical flask with baffles. Kanamycin (25 mg/l) was added.

Culturing was carried out at 33°C and 80% atmospheric humidity.

After 72 hours, the OD was determined at a measurement wavelength of 660 nm with a Biomek 1000 (Beckmann 10 Instruments GmbH, Munich). The amount of L-lysine and of L-valine formed was determined with an amino acid analyzer from Eppendorf-BioTronik (Hamburg, Germany) by ion exchange chromatography and post-column derivatization with ninhydrin detection.

15 The results of the experiment are shown in tables 1 and 2.

Table 1

Strain	OD(660)	Lysine HCl g/l
DSM5715	7.5	13.01
DSM5715::pCR2.1lysR2int	7.2	14.68

Table 2

Strain	OD(660)	Valine g/l
FERM BP-1763	12.1	7.49
FERM BP-1763::pCR2.1lysR2int	13.4	10.90

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; New nucleotide sequences which code for the lysR2 gene

&lt;130&gt; 000181 BT

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10 &lt;141&gt;

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&lt;222&gt; (232)..(1161)

25 &lt;223&gt; lysR2 gene

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Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu  
85 90 95

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5 gtc ccc gaa ctt atc cga aca ttc cgc gcc gaa cac ccc aac gta gaa 621  
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 115 120 125 130

10 ttc caa ctc cac caa gcg gca gca atg ctc ctg gta gat cgt gtt ttg 669  
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 135 140 145

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25 Val Leu Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile  
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30 Val Ala Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp  
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35 Pro Glu Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr  
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40 Val Glu Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg  
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Val Leu Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala  
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45 Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu  
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Ala Leu Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln  
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Gly Glu Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met  
 195 200 205

50 Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu  
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Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr  
 225 230 235 240

Val Ala Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met  
 245 250 255

Asp Asp Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser  
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 Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly  
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 tccgaacatt cccgcggaa cacccaaag tagaaatcca actccaccaa gggcagcaaa 180  
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The following figures are attached:

Figure 1: Map of the plasmid pCR2.1lysR2int.

The abbreviations and designations used have the following meaning.

KmR: Kanamycin resistance gene

EcoRI: Cleavage site of the restriction enzyme EcoRI

lysR2int: Internal fragment of the lysR2 gene

ColE1 ori: Replication origin of the plasmid ColE1